SEQUENCE LISTING

(1) GENERAL	INFORMATION:
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- (i) APPLICANT: Bucala, Richard J. et al.
- (ii) TITLE OF INVENTION: Inhibition of Migration Inhibitory Factor in the Treatment of Diseases Involving Cytokine-Mediated Toxicity
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS
 - (B) STREET: 1155 Avenue of the Americas (C) CITY: New York

 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036-2711
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible

 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/243,342
 - (B) FILING DATE: 16-MAY-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7815-008
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212 790-9090
 - (B) TELEFAX: 212 869-8864/9741
 - (C) TELEX: 66141 PENNIE
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCCTA	TGT	TCATCGTGAA	CACCAATGTT	CCCCGCGCCT	CCGTGCCAGA	GGGGTTTCTG	60
TCGGAGC	TCA	CCCAGCAGCT	GGCGCAGGCC	ACCGGCAAGC	CCGCACAGTA	CATCGCAGTG	120
CACGTGG	TCC	CGGACCAGCT	CATGACTTTT	AGCGGCACGA	ACGATCCCTG	CGCCCTCTGC	180
AGCCTGC	ACA	GCATCGGCAA	GATCGGTGGT	GCCCAGAACC	GCAACTACAG	TAAGCTGCTG	240
TGTGGCC	TGC	TGTCCGATCG	CCTGCACATC	AGCCCGGACC	GGGTCTACAT	CAACTATTAC	300
GACATGA	ACG	CTGCCAACGT	GGGCTGGAAC	GGTTCCACCT	TCGCTTGA		348

(2) INFORMATION FOR SEQ ID NO:2:

1 11 :

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCCGATGT TCATCGTAAA CACCAACGTG CCCCGCGCCT CCGTGCCGGA CGGGTTCCTC 60 TCCGAGCTCA CCCAGCAGCT GGCGCAGGCC ACCGGCAAGC CCCCCCAGTA CATCGCGGTG 120 CACGTGGTCC CGGACCAGCT CATGGCCTTC GGCGGCTCCA GCGAGCCGTG CGCGCTCTGC 180 AGCCTGCACA GCATCGGCAA GATCGGCGGC GCGCAGAACC GCTCCTACAG CAAGCTGCTG 240 TGCGGCCTGC TGGCCGAGCG CCTGCGCATC AGCCCGGACA GGGTCTACAT CAACTATTAC 300 GACATGAACG CGGCCAGTGT GGGCTGGAAC AACTCCACCT TCGCCTAA 348

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCATGCCTAT GTTCATCGTG AACACCAATG TTCCCCGCGC CTCCGTGCCA GAGGGGTTTC 60 TGTCGGAGCT CACCCAGCAG CTGGCGCAGG CCACCGGCAA GCCCGCACAG TACATCGCAG 120 TGCACGTGGT CCCGGACCAG CTCATGACTT TTAGCGGCAC GAACGATCCC TGCGCCCTCT 180 GCAGCCTGCA CAGCATCGGC AAGATCGGTG GTGCCCAGAA CCGCAACTAC AGTAAGCTGC 240 300 TGTGTGGCCT GCTGTCCGAT CGCCTGCACA TCAGCCCGGA CCGCTCCTAC AGCAAGCTGC TGTGCGGCCT GCTGGCCGAG CGCCTGCGCA TCAGCCCGGA CCGGGTCTAC ATCAACTATT 360 ACGACATGAA CGCTGCCAAC GTGGGCTGGA ACGGTTCCAC CAGGGTCTAC ATCAACTATT 420 ACGACATGAA CGCGGCCAGT GTGGGCTGGA ACAACTCCAC CTTCGCTTGA GTCCTGGCCC 480 CACTTACCTG CACCGCTGTT C 501

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids

 - (B) TYPE: amino acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro 1 10 15

Glu Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly 20 25 30

Lys Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met 35 40 45

Thr Phe Ser Gly Thr Asn Asp Pro Cys Ala Leu Cys Ser Leu His Ser 50 55 60

Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu 65 70 75 80

Cys Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr 85 90 95

Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser 100 105 110

Thr Phe Ala 115

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro 1 5 10 15

Asp Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly 20 25 30

Lys Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met 35 40 45

Ala Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser 50 55 60

Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu 65 70 75 80

Cys Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr 85 90 95

Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser 100 105 110

Thr Phe Ala

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	Ala Lys Lys Gly Ala Val Gly Gly Ile 1 5	
(2)	INFORMATION FOR SEQ ID NO:7:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: peptide	
	<pre>(ix) FEATURE: (A) NAME/KEY: Peptide (B) LOCATION: 15 (D) OTHER INFORMATION: /label= X</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
	Ile Xaa His Asn Thr Val Ala Thr Glu Ile Ser Gly Tyr Asn Xaa Ala 1 5 10 15	
	Met	
(2)	INFORMATION FOR SEQ ID NO:8:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
CCAT	TATGCCG ATGTTCATCG TAAACAC	27
(2)	INFORMATION FOR SEQ ID NO:9:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: DNA	
÷	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
GGA <i>l</i>	AGCGGAT TCTCGGCGTC CTAGGC	26
(2)	INFORMATION FOR SEQ ID NO:10:	

	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 		
	(ii) MOLECULE TYPE: DNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:		
CCAT	IGCCTAT GTTCATCGTG		20
(2)	INFORMATION FOR SEQ ID NO:11:		
\- /	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown		
	(ii) MOLECULE TYPE: DNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:		
GTG	AATGGAC GTGGCGACAA G	21	
(2)	INFORMATION FOR SEQ ID NO:12:		
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 		
	(ii) MOLECULE TYPE: DNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:		
ССТС	GGTCGCA GAGTTTAA		18
(2)	INFORMATION FOR SEQ ID NO:13:		
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 		
	(ii) MOLECULE TYPE: DNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:		
CCAC	GAACGTT CCTTGTCT		18
(2)	INFORMATION FOR SEQ ID NO: 14:		
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single		

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GTGGCCGCT CTAGGCACCA	20
(2) INFORMATION FOR SEQ ID NO:15:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
GGGGGACTTG GGATTCCGGT	20
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
GCGGAGTCCG GGCAGGTCTA	20
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GGAGTGTCTC GGTCGGGGGG	20